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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: markspencer

Timestamp: [year=2008; month=9; day=16; hr=8; min=29; sec=11; ms=981; ]

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Reviewer Comments:

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

Numeric identifier <160> must reflect the total number of sequences in the sequence listing. There are only 226 sequences in this sequence listing but, <160> states there are 229. Please make all necessary changes

<210> 129

<212> PRT

<213> Artificial Sequence

<220>

<223> VEGFR-1 derived peptides

<400> 129

Lys Leu Leu Arg Gly His Thr Leu Val

Numeric identifier "<211> Length" is mandatory for each SEQ ID number.

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Application No: 10511384

Version No: 3.0

Input Set:

Output Set:

Started: 2008-08-12 14:55:48.277

Finished: 2008-08-12 14:55:50.653

Elapsed: 0 hr(s) 0 min(s) 2 sec(s) 376 ms

Total Warnings: 218

Total Errors: 3

No. of SeqIDs Defined: 229

Actual SeqID Count: 226

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (1)
W 213	Artificial or Unknown found in <213> in SEQ ID (2)
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (4)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (6)
W 213	Artificial or Unknown found in <213> in SEQ ID (7)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)
W 213	Artificial or Unknown found in <213> in SEQ ID (9)
W 213	Artificial or Unknown found in <213> in SEQ ID (10)
W 213	Artificial or Unknown found in <213> in SEQ ID (11)
W 213	Artificial or Unknown found in <213> in SEQ ID (12)
W 213	Artificial or Unknown found in <213> in SEQ ID (13)
W 213	Artificial or Unknown found in <213> in SEQ ID (14)
W 213	Artificial or Unknown found in <213> in SEQ ID (15)
W 213	Artificial or Unknown found in <213> in SEQ ID (16)
W 213	Artificial or Unknown found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (18)
W 213	Artificial or Unknown found in <213> in SEQ ID (27)
W 213	Artificial or Unknown found in <213> in SEQ ID (28)

**Input Set:**

**Output Set:**

**Started:** 2008-08-12 14:55:48.277  
**Finished:** 2008-08-12 14:55:50.653  
**Elapsed:** 0 hr(s) 0 min(s) 2 sec(s) 376 ms  
**Total Warnings:** 218  
**Total Errors:** 3  
**No. of SeqIDs Defined:** 229  
**Actual SeqID Count:** 226

Error code	Error Description
	This error has occurred more than 20 times, will not be displayed
E 249	Order Sequence Error <210> -> <212>; Expected Mandatory Tag: <211> in SEQID ( 129 )
E 252	Calc# of Seq. differs from actual; 229 seqIds defined; count=226
E 250	Structural Validation Error; Sequence listing may not be indexable

# SEQUENCE LISTING

<110> Center for Genetic Engineering and Biotechnology

<120> Antiangiogenic active immunotherapies

<130> 976-19 PCT/US/RCE

<140> 10/511,384

<141> 2004-10-15

<150> CU 2002/0076

<151> 2002-04-15

<160> 229

<170> PatentIn version 3.4

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<213> Artificial Sequence

<220>

<223> primer

<400> 1

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<220>

<223> primer

<400> 2

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<210> 3

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<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 3

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<210> 4

<211> 30

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<220>



<223> primer

<400> 18

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19

<210> 19

<211> 147

<212> PRT

<213> Homo Sapiens

<400> 147

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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly  
20 25 30

Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Glu Ile Glu Pro Glu  
100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
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Pro Arg Arg  
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<210> 20

<211> 444

<212> DNA

<213> Homo Sapiens

<400> 20

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gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180

atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgccctg 240  
atgcatgacg ggggctgctg caatgacgag ggctggagt gtgtgccac tgaggagtcc 300  
aacatcacca tgcagattat gcggatcaaa cctcaccaag gccagcacat aggagagatg 360  
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aaatgtgaca agccgaggcg gtga 444

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<212> PRT  
<213> Homo Sapiens

<400> 147

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20 25 30  
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln  
35 40 45  
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu  
50 55 60  
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu  
65 70 75 80  
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro  
85 90 95  
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Ala Ile Ala Pro Ala  
100 105 110  
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys  
115 120 125  
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys  
130 135 140  
Pro Arg Arg  
145

<210> 22  
<211> 444  
<212> DNA  
<213> Homo Sapiens

<400> 22

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 gtgaagttca tggatgtcta tcagcgcagc tactgccatc caatcgagac cctggtggac 180  
 atcttccagg agtaccctga tgagatcgag tacatcttca agccatcctg tgtgcccctg 240  
 atgcgatgcg ggggctgctg caatgacgag ggcctggagt gtgtgcccac tgaggagtcc 300  
 aacatcacca tgcagattat ggcaatcgca cctgcacaag gccagcacat aggagagatg 360  
 agcttcctac agcacaacaa atgtgaatgc agaccaaaga aagatagagc aagacaagaa 420  
 aaatgtgaca agccgaggcg gtaa 444

<210> 23  
 <211> 314  
 <212> PRT  
 <213> Homo Sapiens  
 <400> 314

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 Thr Arg Ala Ala Ser Val Gly Leu Pro Ser Val Ser Leu Asp Leu Pro  
 20 25 30  
 Arg Leu Ser Ile Gln Lys Asp Ile Leu Thr Ile Lys Ala Asn Thr Thr  
 35 40 45  
 Leu Gln Ile Thr Cys Arg Gly Gln Arg Asp Leu Asp Trp Leu Trp Pro  
 50 55 60  
 Asn Asn Gln Ser Gly Ser Glu Gln Arg Val Glu Val Thr Glu Cys Ser  
 65 70 75 80  
 Asp Gly Leu Phe Cys Lys Thr Leu Thr Ile Pro Lys Val Ile Gly Asn  
 85 90 95  
 Asp Thr Gly Ala Tyr Lys Cys Phe Tyr Arg Glu Thr Asp Leu Ala Ser  
 100 105 110  
 Val Ile Tyr Val Tyr Val Gln Asp Tyr Arg Ser Pro Phe Ile Ala Ser  
 115 120 125  
 Val Ser Asp Gln His Gly Val Val Tyr Ile Thr Glu Asn Lys Asn Lys  
 130 135 140  
 Thr Val Val Ile Pro Cys Leu Gly Ser Ile Ser Asn Leu Asn Val Ser  
 145 150 155 160  
 Leu Cys Ala Arg Tyr Pro Glu Lys Arg Phe Val Pro Asp Gly Asn Arg  
 165 170 175  
 Ile Ser Trp Asp Ser Lys Lys Gly Phe Thr Ile Pro Ser Tyr Met Ile

180	185	190
Ser Tyr Ala Gly Met Val Phe Cys Glu Ala Lys Ile Asn Asp Glu Ser		
195	200	205
Tyr Gln Ser Ile Met Tyr Ile Val Val Val Val Gly Tyr Arg Ile Tyr		
210	215	220
Asp Val Val Leu Ser Pro Ser His Gly Ile Glu Leu Ser Val Gly Glu		
225	230	235
Lys Leu Val Leu Asn Cys Thr Ala Arg Thr Glu Leu Asn Val Gly Ile		
245	250	255
Asp Phe Asn Trp Glu Tyr Pro Ser Ser Lys His Gln His Lys Lys Leu		
260	265	270
Val Asn Arg Asp Leu Lys Thr Gln Ser Gly Ser Glu Met Lys Lys Phe		
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290	295	300
Tyr Thr Cys Ala Ala Ser Ser Gly Leu Met		
305	310	

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 <212> DNA  
 <213> Homo Sapiens

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cttacaatta aggctaatac aactcttcaa attacttgca ggggacagag ggacttggac	180
tggctttggc ccaataatca gagtggcagt gagcaaaggg tggaggtgac tgagtgcagc	240
gatggcctct tctgtaagac actcacaatt ccaaaagtga tcggaaatga cactggagcc	300
tacaagtgct tctaccgga aactgacttg gcctcgggtca tttatgtcta tgttcaagat	360
tacagatctc catttattgc ttctgttagt gaccaacatg gagtcgtgta cattactgag	420
aacaaaaaca aaactgtggt gattccatgt ctcgggtcca tttcaaactt caacgtgtca	480
ctttgtgcaa gataccaga aaagagattt gttcctgatg gtaacagaat ttctggggac	540
agcaagaagg gctttactat tcccagctac atgatcagct atgctggcat ggtcttctgt	600
gaagcaaaaa ttaatgatga aagttaccag tctattatgt acatagttgt cgttgtaggg	660
tataggattt atgatgtggt tctgagtcg tctcatggaa ttgaactatc tgttgagaa	720

aagcttgtct taaattgtac agcaagaact gaactaaatg tggggattga cttcaactgg 780  
gaataccctt cttcgaagca tcagcataag aaacttgtaa accgagacct aaaaaccag 840  
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gaccaaggat tgtacacctg tgcagcatcc agtgggctga tga 943

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<211> 611  
<212> PRT  
<213> Homo sapiens

<400> 611

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Asn Leu Glu Ile Ile Ile Leu Val Gly Thr Ala Val Ile Ala Met Phe  
20 25 30

Phe Trp Leu Leu Leu Val Ile Ile Leu Arg Thr Val Lys Arg Ala Asn  
35 40 45

Gly Gly Glu Leu Lys Thr Gly Tyr Leu Ser Ile Val Met Asp Pro Asp  
50 55 60

Glu Leu Pro Leu Asp Glu His Cys Glu Arg Leu Pro Tyr Asp Ala Ser  
65 70 75 80

Lys Trp Glu Phe Pro Arg Asp Arg Leu Lys Leu Gly Lys Pro Leu Gly  
85 90 95

Arg Gly Ala Phe Gly Gln Val Ile Glu Ala Asp Ala Phe Gly Ile Asp  
100 105 110

Lys Thr Ala Thr Cys Arg Thr Val Ala Val Lys Met Leu Lys Glu Gly  
115 120 125

Ala Thr His Ser Glu His Arg Ala Leu Met Ser Glu Leu Lys Ile Leu  
130 135 140

Ile His Ile Gly His His Leu Asn Val Val Asn Leu Leu Gly Ala Cys  
145 150 155 160

Thr Lys Pro Gly Gly Pro Leu Met Val Ile Val Glu Phe Cys Lys Phe  
165 170 175

Gly Asn Leu Ser Thr Tyr Leu Arg Ser Lys Arg Asn Glu Phe Val Pro  
180 185 190

Tyr Lys Thr Lys Gly Ala Arg Phe Arg Gln Gly Lys Asp Tyr Val Gly  
195 200 205

Ala Ile Pro Val Asp Leu Lys Arg Arg Leu Asp Ser Ile Thr Ser Ser  
210 215 220

Gln Ser Ser Ala Ser Ser Gly Phe Val Glu Glu Lys Ser Leu Ser Asp  
225 230 235 240

Val Glu Glu Glu Glu Ala Pro Glu Asp Leu Tyr Lys Asp Phe Leu Thr  
245 250 255

Leu Glu His Leu Ile Cys Tyr Ser Phe Gln Val Ala Lys Gly Met Glu  
260 265 270

Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala Arg Asn  
275 280 285

Ile Leu Leu Ser Glu Lys Asn Val Val Lys Ile Cys Asp Phe Gly Leu  
290 295 300

Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly Asp Ala  
305 310 315 320

Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Thr Ile Phe Asp Arg Val  
325 330 335

Tyr Thr Ile Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu Trp Glu  
340 345 350

Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Lys Ile Asp Glu  
355 360 365

Glu Phe Cys Arg Arg Leu Lys Glu Gly Thr Arg Met Arg Ala Pro Asp  
370 375 380

Tyr Thr Thr Pro Glu Met Tyr Gln Thr Met Leu Asp Cys Trp His Gly

385											390											395											400
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				405								410								415													
Asn	Leu	Leu	Gln	Ala	Asn	Ala	Gln	Gln	Asp	Gly	Lys	Asp	Tyr	Ile	Val																		
				420								425								430													
Leu	Pro	Ile	Ser	Glu	Thr	Leu	Ser	Met	Glu	Glu	Asp	Ser	Gly	Leu	Ser																		
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Leu	Pro	Thr	Ser	Pro	Val	Ser	Cys	Met	Glu	Glu	Glu	Glu	Val	Cys	Asp																		
				450								455								460													
Pro	Lys	Phe	His	Tyr	Asp	Asn	Thr	Ala	Gly	Ile	Ser	Gln	Tyr	Leu	Gln																		
465								470								475								480									
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				485								490								495													
Ile	Pro	Leu	Glu	Glu	Pro	Glu	Val	Lys	Val	Ile	Pro	Asp	Asp	Asn	Gln																		
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Thr	Asp	Ser	Gly	Met	Val	Leu	Ala	Ser	Glu	Glu	Leu	Lys	Thr	Leu	Glu																		
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Asp	Arg	Thr	Lys	Leu	Ser	Pro	Ser	Phe	Gly	Gly	Met	Val	Pro	Ser	Lys																		
530								535								540																	
Ser	Arg	Glu	Ser	Val	Ala	Ser	Glu	Gly	Ser	Asn	Gln	Thr	Ser	Gly	Tyr																		
545								550								555								560									
Gln	Ser	Gly	Tyr	His	Ser	Asp	Asp	Thr	Asp	Thr	Thr	Val	Tyr	Ser	Ser																		
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Glu	Glu	Ala	Glu	Leu	Leu	Lys	Leu	Ile	Glu	Ile	Gly	Val	Gln	Thr	Gly																		
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Ser	Thr	Ala	Gln	Ile	Leu	Gln	Pro	Asp	Ser	Gly	Thr	Thr	Leu	Ser	Ser																		
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gtagaagaag aggaagctcc tgaagatctg tataaggact tcctgacctt ggagcatctc	780
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